

WEST Search History

DATE: Tuesday, November 16, 2004

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L4	cd11b same (189 or 316 or 332)	12
<input type="checkbox"/>	L3	xiong-jian-ping.in.	6
<input type="checkbox"/>	L2	li-rui.in.	13
<input type="checkbox"/>	L1	arnaout-\$-amin.in.	15

END OF SEARCH HISTORY

=> d his

(FILE 'HOME' ENTERED AT 09:31:07 ON 16 NOV 2004)

FILE 'STNGUIDE' ENTERED AT 09:32:13 ON 16 NOV 2004

FILE 'DISSABS, IMOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, MEDICONF,
OCEAN, PAPERCHEM2, PASCAL, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,
ADISNEWS, ANABSTR, ANTE, AQUALINE, BIOBUSINESS, ...' ENTERED AT 09:32:27
ON 16 NOV 2004

L1	E ARNAOUT M AMIN?/AU
	396 S E1 OR E2 OR E10
	E LI RUI?/AU
L2	2 S E1 OR E2
	E XIONG JIAN-PING?/AU
	E XIONG 'JIAN-PING'?/AU
	E XIONG JIANPING?/AU
L3	21 S E1 OR E2
L4	41 S CD11B (S) ILE
L5	19 S L4 (S) (OPEN OR CLOSE OR ACTIVE OR NEO? OR CONFORMATION)
L6	14 DUP REM L5 (5 DUPLICATES REMOVED)
L7	8 S L4 (S) (316 OR 189)

=>

L6 ANSWER 8 OF 14 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on
STN

ACCESSION NUMBER: 2000:943978 SCISEARCH

THE GENUINE ARTICLE: 381AH

TITLE: An isoleucine-based allosteric switch controls affinity
and shape shifting in integrin CD11b A-domain

AUTHOR: Xiong J P; Li R; Essafi M; Stehle T; Arnaout M A (Reprint)

CORPORATE SOURCE: MASSACHUSETTS GEN HOSP, RENAL UNIT, LEUKOCYTE BIOL &
INFLAMMAT PROGRAM, 149 13TH ST, CHARLESTOWN, MA 02129
(Reprint); MASSACHUSETTS GEN HOSP, RENAL UNIT, LEUKOCYTE
BIOL & INFLAMMAT PROGRAM, CHARLESTOWN, MA 02129; HARVARD
UNIV, SCH MED, CHARLESTOWN, MA 02129

COUNTRY OF AUTHOR: USA

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (8 DEC 2000) Vol. 275,
No. 49, pp. 38762-38767.

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC,
9650 ROCKVILLE PIKE, BETHESDA, MD 20814.

ISSN: 0021-9258.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE

LANGUAGE: English

REFERENCE COUNT: 37

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In response to cell activation signals, integrins switch from a low to
a high affinity state. Physiologic ligands bind to integrins through a von
Willebrand Factor A-type domain. Crystallographic studies revealed two
conformations of this domain, 'closed' and 'open.'
The latter crystallizes in complex with a pseudoligand or ligand,
suggesting that it represents the high affinity state; data linking
structure and activity are lacking however. In this communication, we
expressed stable low and high affinity forms of integrin **CD11b**
A-domain and determined their binding isotherms and crystal structures.
The low affinity form, generated by deleting an N-terminal extension
extrinsic to the domain, did not bind to physiologic ligands, and
crystallized in the closed **conformation**. The high affinity form
was generated by either deleting or substituting an invariable C-terminal
Ile(316), wedged into a hydrophobic socket in the closed form, but
displaced from it in the **open** structure. Both mutants
crystallized in the **open conformation**, and the **Ile316**
--> Gly-modified integrin displayed high affinity. Structural differences
between the low and high affinity forms were detected in solution. These
data establish the structure-function correlates for the **CD11b**
A-domain, and define a ligand-independent isoleucine-based allosteric
switch intrinsic to this domain that controls its **conformation**
and affinity.